

**2131-Pos Board B861****Gene Expression in a 2D System****Eyal Karzbrun<sup>1</sup>**, Alexandra Tayar<sup>1</sup>, Vincent Noireaux<sup>2</sup>, Roy Haim Bar-ziv<sup>1</sup>.<sup>1</sup>Weizmann Institute of Science, Rehovot, Israel, <sup>2</sup>University of Minnesota, Minneapolis, MN, USA.

We designed a new integration scheme for artificial biological systems into solid materials. Inspired by the spatial patterns in morphogenesis and by microelectronics, we developed a biochip on which the protein synthesis and assembly is carried out in spatially segregated micro-compartments.

**2132-Pos Board B862****Designing Highly Tunable Semiflexible Filament Networks****Ronald J. Pandolfi**, Lauren E. Edwards, Linda S. Hirst.

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Stiff or semi-flexible polymers have the potential to generate a diverse family of network-based materials. Such materials differ significantly in structure from those seen in polymeric systems formed from molecules approximated by the freely jointed chain. The solution behavior is well known for specific biological examples such as F-actin, microtubules, DNA etc. under the influence of cross-linking proteins or specific ionic conditions. However, a general picture of phase behavior and the range of accessible structures as a function of flexibility, length, attractive potential, and concentration has not yet emerged as these parameters are often difficult to tune experimentally. Here we show an approach to this problem by modeling filament assembly under the influence of a modified Lennard-Jones potential, and a rich variety of network structures, as seen in biological and synthetic examples, are generated. Our results reveal that previously observed networks of bundles seen in F-actin systems are not unique to certain cross-linkers but occupy a tunable position in the phase diagram. Further modification of filament parameters allows the generation of hierarchically structured networks not seen in flexible polymer systems. Our coarse-grained model, inspired by models of F-actin networks with explicit cross-linkers, greatly expands the accessible parameter space. Approximating the effect of crosslinkers by a Lennard-Jones like potential allows for a more tunable representation of filament attraction and binding. The network phases are observed and diagrammed, showing transitions between distinct structures. Morphological properties of the networks are quantitatively examined using connectivity analysis, radial pair distribution functions and a scaling analysis. Detailing the effects of semi-flexible filament parameters on structure and connectivity in this way provides a roadmap for the design of highly tunable hierarchical networks and aids in the discovery of previously unseen structures for novel bioinspired materials.

**2133-Pos Board B863****Stable Patchy Particles from Immiscible Lipid Mixtures****Dylan Bargteil**, Lea-Laetitia Pontani, Martin Haase, Jasna Brujic.

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We study the phase behavior of immiscible mixtures of phospholipids and cholesterol at the interface of oil-in-water emulsions. Such mixtures spontaneously decompose into domains on the surface of the droplets, similar to the presence of lipid rafts in cells, presenting the possibility of new biomimetic studies without constructing liposomes. Using a microfluidic device we control the production of monodisperse emulsions and map out a ternary immiscibility diagram allowing for the control of various surface morphologies, including spots, stripes, and hemispheres. All morphologies are found to be accessible using only binary mixtures of either cholesterol and DOPC or cholesterol and sphingomyelin. By functionalizing those controlled patterns with biotinylated lipids, we also make useful candidates for directed self-assembly with specific interactions via streptavidin. Using confocal microscopy and image analysis we find that domains grow to a maximum size and then remain stable against coarsening on a timescale of weeks. Surprisingly stability is not compromised by the presence of increasing amounts of salt, indicating that the stabilizing force is not of electrostatic origin. We investigate and discuss the potential driving forces for the stability of the domains and different lipid compositions could lead to different stabilization mechanisms.

**2134-Pos Board B864****Determining Surface Activity and Membrane Interactions of Ranaspumin-2 and an Engineered Derivative, Surfactant Resisting Foam Formation****Carly R. Strelez<sup>1</sup>**, David Wendell<sup>2</sup>, Shelli L. Frey<sup>1</sup>.<sup>1</sup>Chemistry Department, Gettysburg College, Gettysburg, PA, USA, <sup>2</sup>School of Energy, Environmental, Biological and Medical Engineering, University of Cincinnati, Cincinnati, OH, USA.

Ranaspumin-2 (Rsn-2) is a surfactant protein identified as one of the major components of tungara frog foam nests which protects fertilized eggs from

dehydration, temperature changes, and potential pathogens. Unlike chemical detergents, the protective protein does not disrupt cell membranes making it a strong candidate for agricultural applications, save for its foaming upon agitation which can result in wind resistance and reduced coverage. Surfactant Resisting Foam formation (SRFN) protein was engineered to retain the biological compatibility of Rsn2, ultimately the same surface tension reduction, but contains a more flexible hinge point in the clamshell-like structure which reduces foaming. Both Rsn-2 and SRFN exhibited appreciable surface activity down to sub- $\mu\text{g/ml}$  concentrations without a lag time, measured as surface pressure at the air-buffer interface. Mixing and agitation, to model environmental conditions, has limited effect on the surfactant qualities of Rsn-2 and SRFN. Rsn-2 formed a significant amount of foam that dissipated slowly, but mixing did not affect the resultant surface pressure or equilibration time. For SRFN, a protein of equal size, the main effect of agitation was to accelerate the equilibration time of protein adsorbing to the interface; direct agitation led to little foaming. To confirm that the site-direction mutations in the hinge region of SRFN do not enhance the protein's ability to insert into a lipid membrane, we modeled the outer leaflet of the cell membrane using an egg phosphatidylcholine lipid monolayer at the air-buffer interface and saw no insertion as physiologically relevant pressures.

**2135-Pos Board B865****Rapid Formation and Flow Around Staphylococcus Aureus Biofilm Streamers****Min Young Kim<sup>1</sup>**, Knut Drescher<sup>2,3</sup>, Bonnie L. Bassler<sup>3,4</sup>, Howard A. Stone<sup>2</sup>.<sup>1</sup>Department of Chemistry, Princeton University, Princeton, NJ, USA,<sup>2</sup>Department of Mechanical and Aerospace Engineering, PrincetonUniversity, Princeton, NJ, USA, <sup>3</sup>Department of Molecular Biology,Princeton University, Princeton, NJ, USA, <sup>4</sup>Howard Hughes Medical

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Bacterial biofilms are surface-associated conglomerates of bacteria that are highly resistant to antibiotics. These bacterial communities can cause chronic infections in humans by colonizing, for example, medical implants, heart valves, or lungs. *Staphylococcus aureus*, a notorious human pathogen, causes some of the most common biofilm-related infections. Despite the clinical importance of *S. aureus* biofilms, it remains mostly unknown how physical effects, and in particular flow, shape the morphology and growth dynamics of biofilms. Here we use model microfluidic systems to investigate how environmental factors, such as surface geometry, surface chemistry, and fluid flow affect the biofilm development in *S. aureus*. We discovered that *S. aureus* rapidly forms flow-induced, filamentous biofilm streamers and that if surfaces are coated with human blood plasma, streamers appear within minutes and clog the channels more rapidly than if the channels are uncoated. We document and model the deformation of the flow field generated by the streamers. Understanding physical aspects of biofilm formation in *S. aureus* may lead to new approaches for interrupting biofilm formation of this pathogen.

**2136-Pos Board B866****Interfacial Mussel Proteins Characterization with the Surface Forces Apparatus****Eric Danner<sup>1</sup>**, Yajing Kan<sup>2</sup>, Malte Hammer<sup>3</sup>, Jing Yu<sup>4</sup>, Wei Wei<sup>1</sup>,Jacob Israelachvili<sup>1</sup>, J Herbert Waite<sup>1</sup>.<sup>1</sup>UCSB, Santa Barbara, CA, USA, <sup>2</sup>Southeast University, Nanjing, China,<sup>3</sup>Leibniz Institute, Greifswald, Germany, <sup>4</sup>Cal Tech, Pasadena, CA, USA.

The biomaterial that mussels produce to fix themselves to their substrate has become a model system for gleaming insights into effective underwater adhesion. These superficially simple animals are capable of fastening robust organic attachments to chemically diverse substrates such as ceramics, metal oxides, polymers and silicate clays. Proteins from this adhesive material have been purified and characterized resulting in a family of molecules with unusual charges, compositions and post-translational modifications. One of these modifications, dihydroxyphenylalanine (DOPA) as gained traction for being found in a multitude of animal adhesive systems as well as having been shown to have impressive work of adhesion values in simple systems. Proteins from the mussel attachment plaque that are simultaneously found at the interface of the substrate and contain unusually high DOPA content were characterized by the Surface Forces Apparatus. This instrument allows for interactions between surfaces and deposited thin films to be measured. The force distance profiles calculated are sensitive to angstrom resolution and pN forces.

In this talk the results of characterizing interfacial mussel foot proteins by with the surface forces apparatus will be discussed. The effects on adhesion from solution conditions- especially with regard to pH, protein-protein interactions, effects of protein oxidation and reduction, as well as the potential utility of borate protection are shown in a quantitative way.